

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 13:58:46 ; Search time 77 Seconds
(without alignments)
58.871 Million cell updates/sec

Title: US-09-914-213-2

Perfect score: 116

Sequence: 1 GLEISEINEEDIKCEFPDME 22

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	116	100.0	996	4	Q99989	Q99989 homo sapien
2	116	100.0	1481	6	Q9TU02	Q9TU02 macaca neme
3	116	100.0	1481	6	Q9TSP5	Q9TSP5 papio anubi
4	116	100.0	1481	6	Q62573	Q62573 macaca mula
5	110	94.8	1481	6	Q62668	Q62668 macaca mula
6	103	88.8	1481	6	Q9TXX9	Q9TXX9 oryctolagus
7	95	81.9	1466	13	Q98TR8	Q98TR8 bufo bufo (
8	91	78.4	1485	13	P70034	P70034 xenopus lae
9	77	66.4	1503	13	Q73677	Q73677 fundulus he
10	68	58.6	235	6	Q8SPT1	Q8SPT1 pan. troglod
11	67	57.8	1518	13	Q9TAR8	Q9TAR8 salmo salar
12	64	55.2	1490	13	Q98TYS	Q98TYS salmo salar
13	64	55.2	1519	13	Q9W750	Q9W750 salmo salar
14	62	53.4	1511	13	Q91BE2	Q91BE2 fuqu rubrip
15	56	48.3	244	13	Q9DDK8	Q9DDK8 neoturus ma
16	55	47.4	805	13	Q91BA9	Q91BA9 xenopus lae

17	52	44.8	499	17	Q8U3L0	Q8U3L0 pyrococcus
18	51	44.0	50	2	Q06970	Q06970 bacillus su
19	51	44.0	705	16	Q99UK3	Q99UK3 staphylococ
20	50	43.1	205	5	P90631	P90631 eubacteri
21	50	43.1	682	5	Q9N9B8	Q9N9B8 leishmania
22	49	42.2	260	16	Q931M4	Q931M4 staphylococ
23	49	42.2	1680	4	Q9P129	Q9P129 homo sapien
24	48	41.4	154	10	Q9ZR02	Q9ZR02 arabidopsi
25	48	41.4	413	17	Q28445	Q28445 archaeoglob
26	48	41.4	558	16	Q8RH60	Q8RH60 fusobacteri
27	48	41.4	893	4	Q9N212	Q9N212 homo sapien
28	48	41.4	1016	5	Q92585	Q92585 homo sapien
29	48	41.4	1087	5	Q96923	Q96923 dictyostell
30	48	41.4	1928	5	Q9U0H2	Q9U0H2 plasmodium
31	47.5	40.9	230	12	Q9YVZ1	Q9YVZ1 melanoplus
32	47.5	40.9	414	11	Q9DBC1	Q9DBC1 mus musculu
33	47.5	40.9	414	11	Q8R888	Q8R888 mus musculu
34	47.5	40.9	930	10	Q9FMN2	Q9FMN2 arabidopsi
35	47	40.5	1002	10	Q94KS1	Q94KS1 arabidopsi
36	47	40.5	1048	10	Q9LR48	Q9LR48 arabidopsi
37	46.5	40.1	235	16	Q31789	Q31789 bacillus su
38	46.5	40.1	319	10	Q9SK30	Q9SK30 arabidopsi
39	46.5	40.1	338	15	Q91UB9	Q91UB9 human immun
40	46.5	40.1	380	2	Q9X3R3	Q9X3R3 pseudomonas
41	46.5	40.1	903	3	Q9HGM1	Q9HGM1 schizosacch
42	46	39.7	104	16	Q9CR37	Q9CR37 lactococcus
43	46	39.7	232	16	Q9PNS4	Q9PNS4 staphylococ
44	46	39.7	244	10	Q9SRD6	Q9SRD6 arabidopsi
45	46	39.7	304	5	Q16680	Q16680 caenorhabdl

ALIGNMENTS

RESULT 1
Q99989 PRELIMINARY; PRT; 996 AA.

AC Q99989; 01-MAY-1997 (TREMUREL. 03, Created)
DT 01-MAY-1997 (TREMUREL. 03, Last sequence update)
DT 01-JUN-2002 (TREMUREL. 21, Last annotation update)
DE Transmembrane chloride conductor protein (Fragment).
GN CFTR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Scheet, P, Maggi, L, Blandford M.;
RT "The sequence of H. sapiens BAC clone 068P20.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC000111; AAB46352.1; -
DR HSSP: P13569; INBD.
DR InterPro: IPR001140; ABCtransprtTM.
DR Pfam: PF00664; ABC_membrane_2.
DR Pfam: PF00605; ABC_tran; 1.
DR ProDom: PD000006; ABC_transport; 1.
DR TrifRAMS: TRIGR01271; CFTR.protein; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
FT NON_TER 996
SQ SEQUENCE 996 AA; 113334 MW; 0F85321034CA8DBF CRC64;

Query Match 100.0%; Score 116; DB 4; Length 996;
Best Local Similarity 100.0%; Pred. No. 4.6e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLEISEINEEDIKCEFPDME 22

Db 817 GLEISEINEDLKECFDDME 838

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RESULT 2
09TU02 PRELIMINARY: PRT: 1481 AA.
ID 09TU02:
AC 09TU02:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator.
GN CFTR.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Wine J.J., Kuo E., Hurllock G., Glavac D., Dean M.;
RT "CFTR genomic sequences from five primate species.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162400; AAD46905.1; JOINED.
DR EMBL: AF162374; AAD46905.1; JOINED.
DR EMBL: AF162375; AAD46905.1; JOINED.
DR EMBL: AF162376; AAD46905.1; JOINED.
DR EMBL: AF162377; AAD46905.1; JOINED.
DR EMBL: AF162378; AAD46905.1; JOINED.
DR EMBL: AF162379; AAD46905.1; JOINED.
DR EMBL: AF162380; AAD46905.1; JOINED.
DR EMBL: AF162381; AAD46905.1; JOINED.
DR EMBL: AF162382; AAD46905.1; JOINED.
DR EMBL: AF162383; AAD46905.1; JOINED.
DR EMBL: AF162384; AAD46905.1; JOINED.
DR EMBL: AF162385; AAD46905.1; JOINED.
DR EMBL: AF162386; AAD46905.1; JOINED.
DR EMBL: AF162387; AAD46905.1; JOINED.
DR EMBL: AF162388; AAD46905.1; JOINED.
DR EMBL: AF162389; AAD46905.1; JOINED.
DR EMBL: AF162390; AAD46905.1; JOINED.
DR EMBL: AF162391; AAD46905.1; JOINED.
DR EMBL: AF162392; AAD46905.1; JOINED.
DR EMBL: AF162393; AAD46905.1; JOINED.
DR EMBL: AF162394; AAD46905.1; JOINED.
DR EMBL: AF162395; AAD46905.1; JOINED.
DR EMBL: AF162396; AAD46905.1; JOINED.
DR EMBL: AF162397; AAD46905.1; JOINED.
DR EMBL: AF162398; AAD46905.1; JOINED.
DR EMBL: AF162399; AAD46905.1; JOINED.
DR HSSP: P13569; INBD.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transport.
DR InterPro: IPR005291; CAMP_channel.
DR Pfam: PF00664; ABC_membrane_2.
DR Pfam: PF00005; ABC_tran_2.
DR ProDom: PD000006; ABC_transport; 2.
DR SMART: SM00382; AAA; 1.
DR TIGRFS: TIGR00953; 3a01202; 1.
DR TIGRFS: TIGR01271; CFTR_protein; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW ATP-binding; Transmembrane.
SQ SEQUENCE 1481 AA: 168460 MW: A9AE0CC87E267570 CRC64;
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Query Match 100.0%; Score 116; DB 6; Length 1481;
Best Local Similarity 100.0%; Pred. No. 6.8e-08;
Matches 22; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GLEISEINEDLKECFDDME 22
Db 817 GLEISEINEDLKECFDDME 838

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RESULT 3
09TSP5 PRELIMINARY: PRT: 1481 AA.
ID 09TSP5:
AC 09TSP5:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator.
GN CFTR.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RA Wine J.J., Kuo E., Hurllock G., Glavac D., Dean M.;
RT "CFTR genomic sequences from five primate species.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162401; AAD46907.1; JOINED.
DR EMBL: AF162401; AAD46907.1; JOINED.
DR EMBL: AF162402; AAD46907.1; JOINED.
DR EMBL: AF162403; AAD46907.1; JOINED.
DR EMBL: AF162404; AAD46907.1; JOINED.
DR EMBL: AF162405; AAD46907.1; JOINED.
DR EMBL: AF162406; AAD46907.1; JOINED.
DR EMBL: AF162407; AAD46907.1; JOINED.
DR EMBL: AF162408; AAD46907.1; JOINED.
DR EMBL: AF162409; AAD46907.1; JOINED.
DR EMBL: AF162410; AAD46907.1; JOINED.
DR EMBL: AF162411; AAD46907.1; JOINED.
DR EMBL: AF162412; AAD46907.1; JOINED.
DR EMBL: AF162413; AAD46907.1; JOINED.
DR EMBL: AF162414; AAD46907.1; JOINED.
DR EMBL: AF162415; AAD46907.1; JOINED.
DR EMBL: AF162416; AAD46907.1; JOINED.
DR EMBL: AF162417; AAD46907.1; JOINED.
DR EMBL: AF162418; AAD46907.1; JOINED.
DR EMBL: AF162419; AAD46907.1; JOINED.
DR EMBL: AF162420; AAD46907.1; JOINED.
DR EMBL: AF162421; AAD46907.1; JOINED.
DR EMBL: AF162422; AAD46907.1; JOINED.
DR EMBL: AF162423; AAD46907.1; JOINED.
DR EMBL: AF162424; AAD46907.1; JOINED.
DR EMBL: AF162425; AAD46907.1; JOINED.
DR EMBL: AF162426; AAD46907.1; JOINED.
DR HSSP: P13569; INBD.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transport.
DR InterPro: IPR005291; CAMP_channel.
DR Pfam: PF00664; ABC_membrane_2.
DR Pfam: PF00005; ABC_tran_2.
DR ProDom: PD000006; ABC_transport; 2.
DR SMART: SM00382; AAA; 1.
DR TIGRFS: TIGR00953; 3a01202; 1.
DR TIGRFS: TIGR01271; CFTR_protein; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW ATP-binding; Transmembrane.
SQ SEQUENCE 1481 AA: 168474 MW: A9AE0F3BB4192570 CRC64;
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Query Match 100.0%; Score 116; DB 6; Length 1481;
Best Local Similarity 100.0%; Pred. No. 6.8e-08;
Matches 22; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GLEISEINEDLKECFDDME 22
Db 817 GLEISEINEDLKECFDDME 838

RESULT 4
062673

DR	EMBL: AF162357	AAD46904.1	JOINED
DR	EMBL: AF162358	AAD46904.1	JOINED
DR	EMBL: AF162359	AAD46904.1	JOINED
DR	EMBL: AF162360	AAD46904.1	JOINED
DR	EMBL: AF162361	AAD46904.1	JOINED
DR	EMBL: AF162362	AAD46904.1	JOINED
DR	EMBL: AF162363	AAD46904.1	JOINED
DR	EMBL: AF162364	AAD46904.1	JOINED
DR	EMBL: AF162365	AAD46904.1	JOINED
DR	EMBL: AF162366	AAD46904.1	JOINED
DR	EMBL: AF162367	AAD46904.1	JOINED
DR	EMBL: AF162368	AAD46904.1	JOINED
DR	EMBL: AF162369	AAD46904.1	JOINED
DR	EMBL: AF162370	AAD46904.1	JOINED
DR	EMBL: AF162371	AAD46904.1	JOINED
DR	EMBL: AF162372	AAD46904.1	JOINED
DR	EMBL: AF162177	AAF80467.1	-
DR	EMBL: AF162151	AAF80467.1	JOINED
DR	EMBL: AF162152	AAF80467.1	JOINED
DR	EMBL: AF162153	AAF80467.1	JOINED
DR	EMBL: AF162154	AAF80467.1	JOINED
DR	EMBL: AF162155	AAF80467.1	JOINED
DR	EMBL: AF162156	AAF80467.1	JOINED
DR	EMBL: AF162157	AAF80467.1	JOINED
DR	EMBL: AF162158	AAF80467.1	JOINED
DR	EMBL: AF162159	AAF80467.1	JOINED
DR	EMBL: AF162160	AAF80467.1	JOINED
DR	EMBL: AF162161	AAF80467.1	JOINED
DR	EMBL: AF162162	AAF80467.1	JOINED
DR	EMBL: AF162163	AAF80467.1	JOINED
DR	EMBL: AF162164	AAF80467.1	JOINED
DR	EMBL: AF162165	AAF80467.1	JOINED
DR	EMBL: AF162166	AAF80467.1	JOINED
DR	EMBL: AF162167	AAF80467.1	JOINED
DR	EMBL: AF162168	AAF80467.1	JOINED
DR	EMBL: AF162169	AAF80467.1	JOINED
DR	EMBL: AF162170	AAF80467.1	JOINED
DR	EMBL: AF162171	AAF80467.1	JOINED
DR	EMBL: AF162172	AAF80467.1	JOINED
DR	EMBL: AF162173	AAF80467.1	JOINED
DR	EMBL: AF162174	AAF80467.1	JOINED
DR	EMBL: AF162175	AAF80467.1	JOINED
DR	HSSP: AF162176	AAF80467.1	JOINED
DR	HSSP: P13569	1MBD	
DR	InterPro: IPR003593	AAA_Appase	
DR	InterPro: IPR001140	ABCtransportrTM	
DR	InterPro: IPR003439	ABC transportrTM	
DR	InterPro: IPR005291	CAMP_cl_channel	
DR	Pfam: PF00664	ABC_tran	2
DR	Pfam: PF00005	ABC_tran	2
DR	ProDom: PDD00006	ABC_transportr	2
DR	SMART: SM00382	AAA_1	
DR	TIGRFAMS: TIGR00953	3a01202	1
DR	TIGRFAMS: TIGR01271	Cfmr.protein	1
DR	PROSITE: PS00211	ABC_TRANSPORTER	UNKNOWN_1
KW	ATP-binding; Transmembrane		
SQ	SEQUENCE 1481 AA; 168487 MW; A9AE0F3BB1197570 CRC64;		
Query Match	100.0%;	Score 116;	DB 6;
Best Local Similarity	100.0%;	Pred. No. 6,8e-08;	
Matches 22;	Conservative 0;	Mismatches 0;	Indels 0;
Gaps 0;			
0Y	1 GLEISEINEDLKCFPDME 22		
Db	817 GLEISEINEDLKCFPDME 838		
RESULT 5			
ID	062668		
AC	062668	PRELIMINARY;	PRT; 1481 AA.
DT	01-AUG-1998	(TREMBlrel. 07, Created)	
DT	01-AUG-1998	(TREMBlrel. 07, Last sequence update)	

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DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update).
DE Cystic fibrosis transmembrane conductance regulator.
GN CFTR.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98191731; PubMed=9530627;
RA Wine J.J., Glavac D., Hurlock G., Robinson C., Lee M., Potocnik U.,
RA Ravnik-Glavac M., Dean M.;
RT "Genomic DNA sequence of Rhesus (M. mulatta) cystic fibrosis (CFTR)
RT gene."
RL Mamm. Genome 9:301-305(1998).
DR EMBL; AF013753; AAC14011.1; -.
DR HSSP; P13569; INBD.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABCtransportTM.
DR InterPro; IPR005291; CAMP_cl_channel.
DR Pfam; PF00664; ABC_membrane; 2.
DR ProDom; PD000006; ABC_transport; 2.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMS; TIGR00953; 3a01202; 1.
DR TIGRFAMS; TIGR01271; CFTR_protein; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
DR ATP-binding; Transmembrane.
SQ SEQUENCE 1481 AA; 168454 MW; 9D204B89F37B7699 CRC64;

Query Match 94.8%; Score 110; DB 6; Length 1481;
Best Local Similarity 95.5%; Pred. No. 4.8e-07;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEISEINEDLKECFDDME 22
DB 817 GLEISEINEDLKECFDDME 838

RESULT 6
Q9TXX9 PRELIMINARY; PRT; 1481 AA.
AC Q9TXX9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Chloride channel.
GN CFTR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BREED NEW ZEALAND WHITE; TISSUE=CORNEA;
RA Rae J.L.;
RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF189720; AAF01067.1; -.
DR HSSP; P13569; INBD.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABCtransportTM.
DR InterPro; IPR005291; CAMP_cl_channel.
DR InterPro; IPR003439; ABC_transport.
DR Pfam; PF00664; ABC_membrane; 2.
DR ProDom; PD000006; ABC_transport; 2.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMS; TIGR00953; 3a01202; 1.
DR TIGRFAMS; TIGR01271; CFTR_protein; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
DR ATP-binding; Transmembrane.
SQ SEQUENCE 1481 AA; 168454 MW; 9D204B89F37B7699 CRC64;

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KW ATP-binding.
SQ SEQUENCE 1481 AA; 168041 MW; 1B217AAE75DDE8A CRC64;

Query Match 88.8%; Score 103; DB 6; Length 1481;
Best Local Similarity 86.4%; Pred. No. 4.7e-06;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEISEINEDLKECFDDME 22
DB 817 GLEISEINEDLKECFDDME 838

RESULT 7
Q98TR8 PRELIMINARY; PRT; 1466 AA.
AC Q98TR8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator.
GN CFTR.
OS Bufo bufo (European toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Bufo.
OX NCBI_TaxID=8384;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=BELLY SKIN;
RA Amstrup J., Hyild Larsen E.;
RT "Cloning of CFTR from Bufo bufo, Linnaeus, 1758."
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY026761; AAK07685.1; -.
DR EMBL; AY026761; AAK07685.1; -.
DR HSSP; P13569; INBD.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABCtransportTM.
DR InterPro; IPR005291; CAMP_cl_channel.
DR InterPro; IPR003439; ABC_transport.
DR Pfam; PF00664; ABC_membrane; 2.
DR ProDom; PD000006; ABC_transport; 2.
DR SMART; SM00382; AAA; 2.
DR TIGRFAMS; TIGR00953; 3a01202; 1.
DR TIGRFAMS; TIGR01271; CFTR_protein; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
DR ATP-binding; Transmembrane.
SQ SEQUENCE 1466 AA; 165997 MW; EB692EC3C611C169 CRC64;

Query Match 81.9%; Score 95; DB 13; Length 1466;
Best Local Similarity 85.7%; Pred. No. 6.3e-05;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LEISEINEDLKECFDDME 22
DB 812 LEISEINEDLKECFDDME 832

RESULT 8
P70034 PRELIMINARY; PRT; 1485 AA.
AC P70034;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator (Fragment).
GN CFTR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96411723; PubMed=8810276;

```

RA Price M.P., Ishihara H., Sheppard D.N., Welsh M.J.;
 RT "Function of Xenopus cystic fibrosis transmembrane conductance
 RT regulator (CFTR) Cl channels and use of human-Xenopus chimeras to
 RT investigate the pore properties of CFTR.";
 RL J. Biol. Chem. 271:25184-25191(1996).
 DR EMBL: U60209; AAC60023.1; -.
 DR HSSP: P13569; INBD.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR001140; ABCtranspRTM.
 DR InterPro: IPR003439; ABC_transport.
 DR InterPro: IPR005291; CAMP_cl_Channel.
 DR Pfam: PF00664; ABC_membrane; 2.
 DR Pfam: PF00005; ABC_tran; 2.
 DR PRODOM: PD000006; ABC_transportr; 2.
 DR SMART: SM00382; AAA; 2.
 DR TIGRFAMS: TIGR00953; 3a01202; 1.
 DR TIGRFAMS: TIGR01271; CFTR_protein; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
 KW ATP-binding; Transmembrane.
 FT NON_TER 1485 1485
 SO SEQUENCE 1485 AA; 168502 MW; 0BEAF0D2264D5A24 CRC64;

Query Match 78.4%; Score 91; DB 13; Length 1485;
 Best Local Similarity 76.2%; Pred. No. 0.00023;
 Matches 16; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 LEISEINEDLKECFDDME 22
 DB 820 LESEDIINEDLKECFDDTD 840

RESULT 9

ID 073677 PRELIMINARY; PRT: 1503 AA.
 AC 073677;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Cystic fibrosis transmembrane conductance regulator.
 GN CFTR.
 OS Fundulus heteroclitus (Killifish) (Mummichog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Acanthomorphi; Acanthopterygii; Percomorpha; Altheriomorpha;
 OC Cyprinodontiformes; Fundulidae; Fundulus.
 NCBI_TaxID=8078;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98191134; PubMed=9530103;
 RA Slinger T.D., Tucker S.J., Marshall W.S., Higgins C.F.;
 RT "A divergent CFTR homologue: highly regulated salt transport in the
 RT euryhaline teleost F. heteroclitus.";
 RL Am. J. Physiol. 274:C715-C723(1998).
 DR EMBL: AF000271; AAC41271.1; -.
 DR HSSP: P13569; INBD.
 DR InterPro: IPR001140; ABCtranspRTM.
 DR InterPro: IPR003439; ABC_transport.
 DR InterPro: IPR005291; CAMP_cl_Channel.
 DR Pfam: PF00664; ABC_membrane; 2.
 DR Pfam: PF00005; ABC_tran; 2.
 DR PRODOM: PD000006; ABC_transportr; 2.
 DR TIGRFAMS: TIGR00953; 3a01202; 1.
 DR TIGRFAMS: TIGR01271; CFTR_protein; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
 KW Transmembrane.
 SO SEQUENCE 1503 AA; 169250 MW; B95766EEFA205920 CRC64;

Query Match 66.4%; Score 77; DB 13; Length 1503;
 Best Local Similarity 65.0%; Pred. No. 0.023;
 Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 EISEINEDLKECFDDME 22
 :||||:||||:|||||

DB 831 DISEVDEDEMECFADRE 850

RESULT 10

ID 08SPT1 PRELIMINARY; PRT: 235 AA.
 AC 08SPT1;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Cystic fibrosis transmembrane conductance regulatory domain
 DE (Fragment).
 GN CFTR.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yin H., Chen Y., Alendberg G., Reuss L.;
 RT "CFTR-R domain sequence from chimpanzee genomic DNA.";
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF490140; AAM08348.1; -.
 KW Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 235 235
 SO SEQUENCE 235 AA; 26727 MW; 1257A413EBA9DCEF CRC64;

Query Match 58.6%; Score 68; DB 6; Length 235;
 Best Local Similarity 100.0%; Pred. No. 0.07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GLEISEINEDLK 14
 DB 222 GLEISEINEDLK 235

RESULT 11

ID 09IAR8 PRELIMINARY; PRT: 1518 AA.
 AC 09IAR8;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Cystic fibrosis transmembrane conductance regulator II.
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 NCBI_TaxID=8030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21396404; PubMed=11504857;
 RA Chen J.M., Cutler C., Jacques C., Boeuf G., Denamur E., Lecolntre G.,
 RA Mercier B., Gramb G., Ferec C.;
 RT "A Combined Analysis of the Cystic Fibrosis Transmembrane Conductance
 RT Regulator: Implications for Structure and Disease Models.";
 RL Mol. Biol. Evol. 18:1771-1788(2001).
 DR EMBL: AF161070; AAF37801.1; -.
 DR HSSP: P13569; INBD.
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR001140; ABCtranspRTM.
 DR InterPro: IPR003439; ABC_transport.
 DR InterPro: IPR005291; CAMP_cl_Channel.
 DR Pfam: PF00664; ABC_membrane; 2.
 DR Pfam: PF00005; ABC_tran; 2.
 DR PRODOM: PD000006; ABC_transportr; 2.
 DR SMART: SM00382; AAA; 1.
 DR TIGRFAMS: TIGR00953; 3a01202; 1.
 DR TIGRFAMS: TIGR01271; CFTR_protein; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
 KW ATP-binding; Transmembrane.
 SO SEQUENCE 1518 AA; 171136 MW; B3579B15820BA7F4 CRC64;

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RL Mol. Biol. Evol. 18:1771-1788(2001).
DR EMBL: AF155237; AAD38404.1; -.
DR HSSP: P13569; INED.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR001140; ABCtransp1TM.
DR InterPro: IPR003439; ABC_transp1tr.
DR InterPro: IPR005291; CAMP_cl_channel.
DR Pfam: PF00664; ABC_membrane; 2.
DR Pfam: PF00005; ABC_tran; 2.
DR ProDom: PD000006; ABC_transp1tr; 2.
DR SMART: SM00382; AAA; 1.
DR TIGRFAMs: TIGR00953; 3a01202; 1.
DR TIGRFAMs: TIGR01271; CFRP_protein; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW ATP-binding; Transmembrane
SQ SEQUENCE 1519 AA; 171239 MM; F4A67DF22898240C CRC64;

Query Match 55.2%; Score 64; DB 13; Length 1519;
Best Local Similarity 45.0%; Pred. No. 1.6;
Matches 9; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

3 EISEINEDLKECFDDME 22
:||||::|::|::|::|::|
Db 848 DISEVDEQDMEQCFADERE 867

RESULT 14
O91BE2 PRELIMINARY; PRT; 1511 AA.
AC O91BE2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator.
GN CFRP.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
[1]
RN
RP SEQUENCE FROM N.A. PubMed=10958637;
RX MEDLINE=20414757;
RA Davidson H., Taylor M.S., Doherty A., Boyd A.C., Porteous D.J.;
RT "Genomic sequence analysis for Fugu rubripes CFRP and flanking genes in
RL a 60 kb region conserving synteny with 800 kb of human chromosome 7.";
RN Genome Res. 10:1194-1203(2000).
[2]
RN
RP SEQUENCE FROM N.A.
RA Ayele K., Beckstrom-Sternberg S.M., Benjamin B., Blakesley R.W.,
RA Bouffard G.G., Brinkley C., Brooks S., Dietrich N.L., Granite S.,
RA Guan X., Gupta J., Ho S.-L., Idol J.R., Karlins E., Lee-Din S.-O.,
RA Legaspi R., Lim M., Maduro Q.L., Maduro V.B., Mastaglio C.,
RA Mastrian S.D., McCloskey J.C., McDowell J., Pearson R., Prasad A.,
RA Shvachenko Y., Snyder B., Statilipov S., Thomas J.W., Thomas P.J.,
RA Tjongson E.E., Touchman J.W., Tsurgen C., Vogt J.L., Walker M.A.,
RA Wetherly K.D., Zhang L.-H., Green E.D.;
RL "NSC Comparative Sequencing Initiative";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ271361; CAB96905.1; -.
DR EMBL: AC087333; AAL40378.1; -.
DR HSSP: P13569; INED
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR001140; ABCtransp1TM.
DR InterPro: IPR003439; ABC_transp1tr.
DR InterPro: IPR005291; CAMP_cl_channel.
DR Pfam: PF00664; ABC_membrane; 2.
DR Pfam: PF00005; ABC_tran; 2.
DR ProDom: PD000006; ABC_transp1tr; 2.
DR SMART: SM00382; AAA; 1.
DR TIGRFAMs: TIGR00953; 3a01202; 1.
DR TIGRFAMs: TIGR01271; CFRP_protein; 1.

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DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
 KW ATP-binding; Transmembrane.
 SQ SEQUENCE 1511 AA; 170019 MW; 20EC4AC0EA721BB2 CRC64;

Query Match 53.4%; Score 62; DB 13; Length 1511;
 Best Local Similarity 45.0%; Pred. No. 3;
 Matches 9; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

OY 3 EISEINEEDLKECFDWE 22
 :||||:|:|||||:
 DB 839 DISEDVTEDEMEQCFADRD 858

RESULT 15

O9DDK8 PRELIMINARY; PRT; 244 AA.
 AC O9DDK8:
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Cystic fibrosis transmembrane conductance regulator (Fragment).
 GN CFTR.
 OS Necturus maculosus (Mudpuppy) (Waterdog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidae; Proteidae; Necturus.
 OX NCBI_TaxID=42757;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=GALL BLADDER;
 RA Burton B, Torres R.J., Hellmich H.L., Reuss L.;
 RT "Cystic fibrosis transmembrane conductance regulator from Necturus
 maculosus.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF318308; AAC34562.1; -.
 DR HSSP; P13569; INBD.
 KW Transmembrane.
 FT NON_TER 1
 FT NON_TER 244
 SO SEQUENCE 244 AA; 27813 MW; BABDEB8B8C2FD36A CRC64;

Query Match 48.3%; Score 56; DB 13; Length 244;
 Best Local Similarity 84.6%; Pred. No. 3.6;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LEISEINEEDLK 14
 |||:|||||:
 DB 232 LEINEETNEEDLR 244

Search completed: July 16, 2003, 14:03:06
 Job time : 79 secs

